

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

Applicant Name(s): THE GENE POOL, INC.  
Street address: 300 Queen Anne Ave. N., Suite 392  
City: Seattle  
State/Province: Washington  
Country: US  
Postal code/Zip: 98109-4599  
Phone number: (206) 526-8617 Fax number:

(ii) TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
SPECIFIC SEQUENCE COMPOSITION

(iii) NUMBER OF SEQUENCES: 118

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Saliwanchik & Saliwanchik  
(B) STREET: 2421 N.W. 41st St., Suite A-1  
(C) CITY: Gainesville  
(D) STATE: Florida  
(E) COUNTRY: USA  
(F) ZIP: 32606

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bencen, Gerard H  
(B) REGISTRATION NUMBER: 35,746  
(C) REFERENCE/DOCKET NUMBER: GP-100.C1

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (904) 375-8100  
(B) TELEFAX: (904) 372-5800

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

64

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGGATTCC CCA

13

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGGACTTT CCC

13

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGGGACTTT CCG

13

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGGGGACT TTCCA

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAGGGACT TTCCG

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGTTTTTC CCC

13

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGGACTTT CCGCTGGGGA CTTTCCA

27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGGGACTTT CCGCTGGGGA CTTTCCG

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

67

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTGGGGACT TTCCAGGGGA GGTGTG

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTGGGGACT TTCCGGGGAG CGTGGC

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGGGGACT TTCCGGGGAG GCGCGG

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

68

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCTGGGGACT TTCCAGAGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGGGGACT TTCCAGGGGA GCGGTG

26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

69

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTGGGGACT TTCCAGGGAG GCTGCC

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTCCAGGGA GCGGTGGCCT GGGCGGGACT GGG

33

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGTGGCCTGG GCGGGACTGG GGAGTGGCGT CCC

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCT

45

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGCAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid



- (C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCAT

45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGCGTG GCCT

44

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGGCGC GGCT

44

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGAGAGGCGT GGACT

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGCG TGGACT

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

73

- (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTACAGGGGA CTTTCCGCTG GGGACTTTC AGGGAGGCGT GGGGAG

46

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTACAGGGGA CTTTCCGCTG GGGACTTTC AGGGAGGCTG CCT

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTTCCGCTG GGGACTTTC AGGGAGGCGT GGCCTGGGCG GGACTGGG

48

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

74

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTCCAGGGA GGCCTGGCCT GGGCGGGACT GGGGAGTGGC GTCCC

45

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGG

59

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTCCGCTGG GGACTTTCCA GGGAGGCGTG GCCTGGGCGG GACTGGGGAG TGGCGTCCC

59

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGGA 60  
GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TATCACCGCC AGTGGTATTT ATGTCAACAC CGCCAGAGAT AATTTATCAC CGCAGATGGT 60  
T 61

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TATCACCGCA AGGGATAAAT ATCTAACACC GTGCGTGTTG ACTATTTTAC CTCTGGCGGT 60  
GATA 64

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGGA 60  
GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGG 37

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGACTGGG GAGTGGCGTC CC

22

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGTAT CACCGCCAGT GGTATTTATG

60

TCAACACCGC CAGAGATAAT TTATCACCGC AGATGGTTCT GCA

103

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MÅ

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAACCATCTG CGGTGATAAA TTATCTCTGG CGGTGTTGAC ATAAATACCA CTGGCGGTGA

60

TA

62

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

78

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCCAACCA TCTGCGGTGA TAAATTATCT CTGGCGGTGT TGACATAAAT ACCACTGGCG 60

GTGATACTGC A 71

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATCACCGC CAGTGGTATT TATGTCAACA CCGCCAGAGA TAATTTATCA CCGCAGATGG 60

TTG 63

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCGGGGG GATACCCCC G 21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:



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- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGGACTGGG GAGTGGCGTC CCTATCACCG CAAGGGATAA ATATCTAACA CCGTGC GTGT 60

TGACTATTTT ACCTCTGGCG GTGATAGCAT G 91

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAAGGGCGT AACCGAAATC GGTTGAACCG AAACCGGTTA GTATAAAAGC AGA 53

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAGGGAGT AACCGAAAAC GGTCGGGACC GAAAACGGTG TATATAAAAG ATGT 54

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTAGGGTGT AACCGAAAGC GGTCAACCG AAAACGGTGC ATATATAAAG CAAA

54

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTTCAACCG AATTCGGTTG CATG

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGCAACCG ATTTCGGTTG CCTT

24

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TATGCAACCG AAATAGGTTG GGCA

24

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCCTAACCG TTTTCGGTTA CTTG

24

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGACTAACCG TTTTAGGTCA TATT

24

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GACGACTATC CAGCGACCAA GATCAGAGCC AGACACCGGA AACCCCTGCC AC

52

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GACGACACGG TATCCGCTAC TCAGCTTGTT AAACAGCTAC AGCACACCCC CTC

53

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GACGACGACC TGCAGACACC ACAGACACCG CCCAGCCCCT TACAAAGCTG TTCTGTGCAG

60

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 68 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CATACCAAAG CCGTCGCCTT GGGCACCGAA GAAACACAAC CACTAAGTTG TTGCACAGAG 60  
ACTCAGTG 68

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TAATGTAATT GATTGTAATG ACTCTATGTG CAGTACCAGT ACCGTATTCC AGCACCGTGT 60  
CCGTGGGCAC CGCAAAG 77

## (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAGACAACG ATAACCGACC ACCACAAGCA GCGGCCAAAC ACCCCGCCTT GGACAATAGA 60  
ACAGCACGTA CTGCAACTAA 80

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATATGCAAT ACAATGCATT ATACAAACTG GACACATATA TATATTTGTG AAGAAGCATC 60  
AGTAACTGTG GTAGAGGGTC AAGTTGACTA TTATGGTTTA TATTATGTTC ATGAAGGAAT 120  
ACGAACATAT TTTGTGCAGT TTAAAGATGA TGCAGAAAAA TATAGTAAAA ATAAAGTATG 180  
GGAAGTTCAT GCGGGTGGTC AGGTAATATT ATGTCCTACA TCTGTGTTTA GCAGCAACGA 240  
AGTATCCTCT CCTGAAATTA TTAGGC 266

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGGATGTATA AAAAAACATG GATATACAGT GGAAGTGCAG TTTGATGGAG ACATATGCTA 60  
TTAGGCAGCA CTTGGCCAAC CACCCCGCCG CGACC 95

(2) INFORMATION FOR SEQ ID NO:62:

85

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CATGTTTTTT TATACATCCA TATCACCGCC AGTGGTATTT ATGTCAACAC CGCCAGAGAT 60

AATTATCAC CGCAGATGGT T 81

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Ala	Asp	Asp	Asp	Pro	Tyr	Gly	Thr	Gly	Gln	Met	Phe	His	Leu	Asn
1				5					10					15	

Thr	Ala	Leu	Thr	His	Ser	Ile	Phe	Asn	Ala	Glu	Leu	Tyr	Ser	Pro	Glu
		20						25					30		

Ile	Pro	Leu	Ser	Thr	Asp	Gly	Pro	Tyr	Leu	Gln	Ile	Leu	Glu	Gln	Pro
		35					40				45				

Lys	Gln	Arg	Gly	Phe	Arg	Phe	Arg	Tyr	Val	Cys	Glu	Gly	Pro	Ser	His
50					55					60					

Gly	Gly	Leu	Pro	Gly	Ala	Ser	Ser	Glu	Lys	Asn	Lys	Lys	Ser	Tyr	Pro
65				70						75				80	

Gln	Val	Lys	Ile	Cys	Asn	Tyr	Val	Gly	Pro	Ala	Lys	Val	Ile	Val	Gln
			85					90					95		

Leu	Val	Thr	Asn	Gly	Lys	Asn	Ile	His	Leu	His	Ala	His	Ser	Leu	Val
			100				105						110		

86

Gly	Lys	His	Cys	Glu	Asp	Gly	Val	Cys	Thr	Val	Thr	Ala	Gly	Pro	Lys	115	120	125
Asp	Met	Val	Val	Gly	Phe	Ala	Asn	Leu	Gly	Ile	Leu	His	Val	Thr	Lys	130	135	140
Lys	Lys	Val	Phe	Glu	Thr	Leu	Glu	Ala	Arg	Met	Thr	Glu	Ala	Cys	Ile	145	150	155
Arg	Gly	Tyr	Asn	Pro	Gly	Leu	Leu	Val	His	Ser	Asp	Leu	Ala	Tyr	Leu	165	170	175
Gln	Ala	Glu	Gly	Gly	Gly	Asp	Arg	Gln	Leu	Thr	Asp	Arg	Glu	Lys	Glu	180	185	190
Ile	Ile	Arg	Gln	Ala	Ala	Val	Gln	Gln	Thr	Lys	Glu	Met	Asp	Leu	Ser	195	200	205
Val	Val	Arg	Leu	Met	Phe	Thr	Ala	Phe	Leu	Pro	Asp	Ser	Thr	Gly	Ser	210	215	220
Phe	Thr	Arg	Arg	Leu	Glu	Pro	Val	Val	Ser	Asp	Ala	Ile	Tyr	Asp	Ser	225	230	235
Lys	Ala	Pro	Asn	Ala	Ser	Asn	Leu	Lys	Ile	Val	Arg	Met	Asp	Arg	Thr	245	250	255
Ala	Gly	Cys	Val	Thr	Gly	Gly	Glu	Glu	Ile	Tyr	Leu	Leu	Cys	Asp	Lys	260	265	270
Val	Gln	Lys	Asp	Asp	Ile	Gln	Ile	Arg	Phe	Tyr	Glu	Glu	Glu	Glu	Asn	275	280	285
Gly	Gly	Val	Trp	Glu	Gly	Phe	Gly	Asp	Phe	Ser	Pro	Thr	Asp	Val	His	290	295	300
Arg	Gln	Phe	Ala	Ile	Val	Phe	Lys	Thr	Pro	Lys	Tyr	Lys	Asp	Val	Asn	305	310	315
Ile	Thr																	

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met Phe His  
 1 5 10 15  
 Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln  
 20 25 30  
 Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu  
 35 40 45  
 Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly  
 50 55 60  
 Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys  
 65 70 75 80  
 Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val  
 85 90 95  
 Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His  
 100 105 110  
 Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala  
 115 120 125  
 Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile Leu His  
 130 135 140  
 Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu  
 145 150 155 160  
 Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu  
 165 170 175  
 Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly Asp Arg  
 180 185 190  
 Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met  
 195 200 205  
 Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser  
 210 215 220  
 Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile  
 225 230 235 240  
 Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met  
 245 250 255  
 Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu  
 260 265 270  
 Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu  
 275 280 285

Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr  
 290 295 300

Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys  
 305 310 315 320

Asp Ile Asn Ile Thr  
 325

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 268 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Glu Pro Ala Asp Leu Leu Pro Leu Tyr Leu Gln Pro Glu Trp Gly  
 1 5 10 15

Glu Gln Glu Pro Gly Gly Ala Thr Pro Phe Val Glu Ile Leu Glu Gln  
 20 25 30

Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser  
 35 40 45

Ala Gly Ser Ile Pro Gly Glu His Ser Thr Asp Ser Ala Arg Thr His  
 50 55 60

Pro Thr Ile Arg Val Asn His Tyr Arg Gly Pro Gly Arg Val Arg Val  
 65 70 75 80

Ser Leu Val Thr Lys Asp Pro Pro His Gly Pro His Pro His Glu Leu  
 85 90 95

Val Gly Arg His Cys Gln His Gly Tyr Tyr Glu Ala Glu Leu Ser Pro  
 100 105 110

Asp Arg Ser Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys  
 115 120 125

Lys Arg Glu Leu Glu Ala Ala Val Ala Glu Arg Ile Arg Thr Asn Asn  
 130 135 140

Asn Pro Phe Asn Val Pro Met Glu Glu Arg Gly Ala Glu Tyr Asp Leu  
 145 150 155 160

Ser Ala Val Arg Leu Cys Phe Gln Val Trp Val Asn Gly Pro Gly Gly  
 165 170 175  
 Leu Cys Pro Leu Pro Pro Val Leu Ser Gln Pro Ile Tyr Asp Asn Arg  
 180 185 190  
 Ala Pro Ser Thr Ala Glu Leu Arg Ile Leu Pro Gly Asp Arg Asn Ser  
 195 200 205  
 Gly Ser Cys Gln Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val  
 210 215 220  
 Gln Lys Glu Asp Ile Glu Val Arg Phe Trp Ala Glu Gly Trp Glu Ala  
 225 230 235 240  
 Lys Gly Ser Phe Ala Ala Ala Asp Val His Arg Gln Val Ala Ile Val  
 245 250 255  
 Phe Arg Thr Pro Pro Phe Arg Glu Arg Ser Leu Arg  
 260 265

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Asp Asp Leu Phe Pro Leu Ile Phe Pro Ser Glu Pro Ala Gln Ala  
 1 5 10 15  
 Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met  
 20 25 30  
 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly  
 35 40 45  
 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn  
 50 55 60  
 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp  
 65 70 75 80

90

Pro	Pro	His	Arg	Pro	His	Pro	His	Glu	Leu	Val	Gly	Lys	Asp	Cys	Arg	
				85					90					95		
Asp	Gly	Tyr	Tyr	Glu	Ala	Asp	Leu	Cys	Pro	Asp	Arg	Ser	Ile	His	Ser	
				100					105					110		
Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Arg	Asp	Leu	Glu	Gln	
				115					120					125		
Ala	Ile	Ser	Gln	Arg	Ile	Gln	Thr	Asn	Asn	Asn	Pro	Phe	His	Val	Pro	
				130					135					140		
Ile	Glu	Glu	Gln	Arg	Gly	Asp	Tyr	Asp	Leu	Asn	Ala	Val	Arg	Leu	Cys	
				145					150					155		
Phe	Gln	Val	Thr	Val	Arg	Asp	Pro	Ala	Gly	Arg	Pro	Leu	Leu	Leu	Thr	
				165					170					175		
Pro	Val	Leu	Ser	His	Pro	Ile	Phe	Asp	Asn	Arg	Ala	Pro	Asn	Thr	Ala	
				180					185					190		
Glu	Leu	Lys	Ile	Cys	Arg	Val	Asn	Arg	Asn	Ser	Gly	Ser	Cys	Leu	Gly	
				195					200					205		
Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Glu	Asp	Ile	
				210					215					220		
Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	Ala	Arg	Gly	Ser	Phe	Ser	
				225					230					235		
Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro	
				245					250					255		
Tyr	Ala	Asp	Pro	Ser	Leu	Gln										
				260												

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala  
1 5 10 15

Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met  
 20 25 30  
 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly  
 35 40 45  
 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn  
 50 55 60  
 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp  
 65 70 75 80  
 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg  
 85 90 95  
 Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser  
 100 105 110  
 Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln  
 115 120 125  
 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro  
 130 135 140  
 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys  
 145 150 155 160  
 Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro  
 165 170 175  
 Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala  
 180 185 190  
 Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly  
 195 200 205  
 Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile  
 210 215 220  
 Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser  
 225 230 235 240  
 Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro  
 245 250 255  
 Tyr Ala Asp Pro Ser Leu Gln  
 260

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Phe	Pro	Asn	Gln	Asn	Asn	Gly	Ala	Ala	Pro	Gly	Gln	Gly	Pro	Ala	1	5	10	15
Val	Asp	Gly	Gln	Gln	Ser	Leu	Asn	Tyr	Asn	Gly	Leu	Pro	Ala	Gln	Gln	20	25	30	
Gln	Gln	Gln	Leu	Ala	Gln	Ser	Thr	Lys	Asn	Val	Arg	Lys	Lys	Pro	Tyr	35	40	45	
Val	Lys	Ile	Thr	Glu	Gln	Pro	Ala	Gly	Lys	Ala	Leu	Arg	Phe	Arg	Tyr	50	55	60	
Glu	Cys	Glu	Gly	Arg	Ser	Ala	Gly	Ser	Ile	Pro	Gly	Val	Asn	Ser	Thr	65	70	75	80
Pro	Glu	Asn	Lys	Thr	Tyr	Pro	Thr	Ile	Glu	Ile	Val	Gly	Tyr	Lys	Gly	85	90	95	
Arg	Ala	Val	Val	Val	Val	Ser	Cys	Val	Thr	Lys	Asp	Thr	Pro	Tyr	Arg	100	105	110	
Pro	His	Pro	His	Asn	Leu	Val	Gly	Lys	Glu	Gly	Cys	Lys	Lys	Gly	Val	115	120	125	
Cys	Thr	Leu	Glu	Ile	Asn	Ser	Glu	Thr	Met	Arg	Ala	Val	Phe	Ser	Asn	130	135	140	
Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Lys	Asp	Ile	Glu	Ala	Ala	Leu	Lys	145	150	155	160
Ala	Arg	Glu	Glu	Ile	Arg	Val	Asp	Pro	Phe	Lys	Thr	Gly	Phe	Ser	His	165	170	175	
Arg	Phe	Gln	Pro	Ser	Ser	Ile	Asp	Leu	Asn	Ser	Val	Arg	Leu	Cys	Phe	180	185	190	
Gln	Val	Phe	Met	Glu	Ser	Glu	Gln	Lys	Gly	Arg	Phe	Thr	Ser	Pro	Leu	195	200	205	
Pro	Pro	Val	Val	Ser	Glu	Pro	Ile	Phe	Asp	Lys	Lys	Ala	Met	Ser	Asp	210	215	220	
Leu	Val	Ile	Cys	Arg	Leu	Cys	Ser	Cys	Ser	Ala	Thr	Val	Phe	Gly	Asn	225	230	235	240
Thr	Gln	Ile	Ile	Leu	Leu	Cys	Glu	Lys	Val	Ala	Lys	Glu	Asp	Ile	Ser	245	250	255	

Val Arg Phe Phe Glu Glu Lys Asn Gly Gln Ser Val Trp Glu Ala Phe  
                   260                                  265                                  270

Gly Asp Phe Gln His Thr Asp Val His Lys Gln Thr Ala Ile Thr Phe  
                   275                                  280                                  285

Lys Thr Pro Arg Tyr His Thr Leu Asp Ile Thr  
                   290                                  295

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 261 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro  
   1                  5                                  10                                  15

Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Thr Arg Phe Arg  
                   20                                  25                                  30

Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser  
                   35                                  40                                  45

Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe  
                   50                                  55                                  60

Gly Lys Val Lys Ile Arg Thr Thr Leu Val Thr Lys Asn Glu Pro Tyr  
   65                                  70                                  75                                  80

Lys Pro His Pro His Asp Leu Val Gly Lys Gly Cys Arg Asp Gly Tyr  
                   85                                  90                                  95

Tyr Glu Ala Glu Phe Gly Pro Glu Arg Gln Val Leu Ser Phe Gln Asn  
                   100                                  105                                  110

Leu Gly Ile Gln Cys Val Lys Lys Lys Asp Leu Lys Glu Ser Ile Ser  
                   115                                  120                                  125

Leu Arg Ile Ser Lys Lys Asn Pro Phe Asn Val Pro Glu Glu Gln Leu  
                   130                                  135                                  140

94

His Asn Ile Asp Glu Tyr Asp Leu Asn Val Val Arg Leu Cys Phe Gln  
 145 150 155 160  
 Ala Phe Leu Pro Asp Glu His Gly Asn Tyr Thr Leu Ala Leu Pro Pro  
 165 170 175  
 Leu Ile Ser Asn Pro Ile Tyr Asp Asn Arg Ala Pro Asn Thr Ala Glu  
 180 185 190  
 Leu Arg Ile Cys Arg Val Asn Lys Asn Cys Gly Ser Val Lys Gly Gly  
 195 200 205  
 Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Glu  
 210 215 220  
 Val Arg Phe Val Leu Gly Asn Trp Glu Ala Lys Gly Ser Phe Ser Gln  
 225 230 235 240  
 Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro Phe  
 245 250 255  
 Leu Gly Asp Ile Thr  
 260

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 262 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
 

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro  
 1 5 10 15  
 Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Met Arg Phe Arg  
 20 25 30  
 Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser  
 35 40 45  
 Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe  
 50 55 60  
 Gly Lys Val Lys Ile Arg Thr Thr Leu Val Thr Lys Asn Glu Pro Tyr  
 65 70 75 80



[illegible]

(2) INFORMATION FOR SEQ ID NO:71:

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 314 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu  
1 5 10 15

96

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp  
 20 25 30  
 Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn  
 35 40 45  
 Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr  
 50 55 60  
 Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr  
 65 70 75 80  
 Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu  
 85 90 95  
 Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala  
 100 105 110  
 Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val  
 115 120 125  
 Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu  
 130 135 140  
 Arg Ser His Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu Ser  
 145 150 155 160  
 His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr Glu  
 165 170 175  
 Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu Tyr  
 180 185 190  
 Asn Ser Gly Ser Glu Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly  
 195 200 205  
 Ser Asn Phe Leu Thr Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg  
 210 215 220  
 Val Val Asn Leu Glu Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg  
 225 230 235 240  
 Leu Thr Ala Ala Asn Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile  
 245 250 255  
 Asn Lys Phe Val Asn His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala  
 260 265 270  
 Ser Ile Tyr Thr Gln Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met  
 275 280 285  
 Phe Glu Ile Met Phe Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly  
 290 295 300  
 Arg Asp Leu Phe Glu Gln Leu Thr Ser Lys  
 305 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys  
1 5 10 15

Thr

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Asp Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys  
1 5 10 15

Gly Lys Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp  
20 25 30

His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys  
35 40 45

Arg Phe Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr  
50 55 60

Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg  
65 70 75 80

2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409</
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Year	Month	Day	Time	Location	Remarks
1912	March	10	10:30	St. Louis	Left for St. Louis
1912	March	11	11:00	St. Louis	Arrived St. Louis
1912	March	12	12:00	St. Louis	Left St. Louis
1912	March	13	1:00	St. Louis	Arrived St. Louis
1912	March	14	2:00	St. Louis	Left St. Louis
1912	March	15	3:00	St. Louis	Arrived St. Louis
1912	March	16	4:00	St. Louis	Left St. Louis
1912	March	17	5:00	St. Louis	Arrived St. Louis
1912	March	18	6:00	St. Louis	Left St. Louis
1912	March	19	7:00	St. Louis	Arrived St. Louis
1912	March	20	8:00	St. Louis	Left St. Louis
1912	March	21	9:00	St. Louis	Arrived St. Louis
1912	March	22	10:00	St. Louis	Left St. Louis
1912	March	23	11:00	St. Louis	Arrived St. Louis
1912	March	24	12:00	St. Louis	Left St. Louis
1912	March	25	1:00	St. Louis	Arrived St. Louis
1912	March	26	2:00	St. Louis	Left St. Louis
1912	March	27	3:00	St. Louis	Arrived St. Louis
1912	March	28	4:00	St. Louis	Left St. Louis
1912	March	29	5:00	St. Louis	Arrived St. Louis
1912	March	30	6:00	St. Louis	Left St. Louis
1912	March	31	7:00	St. Louis	Arrived St. Louis

- | Year | Month | Day | Time  | Location  | Remarks            |
|------|-------|-----|-------|-----------|--------------------|
| 1912 | March | 10  | 10:30 | St. Louis | Left for St. Louis |
| 1912 | March | 11  | 11:00 | St. Louis | Arrived St. Louis  |
| 1912 | March | 12  | 12:00 | St. Louis | Left St. Louis     |
| 1912 | March | 13  | 1:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 14  | 2:00  | St. Louis | Left St. Louis     |
| 1912 | March | 15  | 3:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 16  | 4:00  | St. Louis | Left St. Louis     |
| 1912 | March | 17  | 5:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 18  | 6:00  | St. Louis | Left St. Louis     |
| 1912 | March | 19  | 7:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 20  | 8:00  | St. Louis | Left St. Louis     |
| 1912 | March | 21  | 9:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 22  | 10:00 | St. Louis | Left St. Louis     |
| 1912 | March | 23  | 11:00 | St. Louis | Arrived St. Louis  |
| 1912 | March | 24  | 12:00 | St. Louis | Left St. Louis     |
| 1912 | March | 25  | 1:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 26  | 2:00  | St. Louis | Left St. Louis     |
| 1912 | March | 27  | 3:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 28  | 4:00  | St. Louis | Left St. Louis     |
| 1912 | March | 29  | 5:00  | St. Louis | Arrived St. Louis  |
| 1912 | March | 30  | 6:00  | St. Louis | Left St. Louis     |
| 1912 | March | 31  | 7:00  | St. Louis | Arrived St. Louis  |

1998

Glu Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu  
           115                          120                          125  
 Leu Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu  
           130                          135                          140  
 Leu Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg  
           145                          150                          155                          160  
 Ala Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly  
                           165                          170                          175  
 Phe Arg Lys Thr Thr  
                           180

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln Val Lys Cys Tyr  
 1                          5                          10                          15  
 Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr Glu Asn Cys Thr  
           20                          25                          30  
 Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu Arg Gln Gly Gln  
           35                          40                          45  
 Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln Arg Gln Asp Phe  
           50                          55                          60  
 Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile Ser Gly Phe Thr  
           65                          70                          75                          80  
 Ala Ser Leu Asp Phe  
                           85

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

100

(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Cys Pro Cys Leu Leu Ile Gly Thr Ser Gly Asn Gly Asn Gln Val Lys  
1 5 10 15

Cys Tyr Ser Phe Arg Val Lys Arg Trp His Asp Arg Asp Lys Tyr His  
20 25 30

His Thr Thr Thr Trp Trp Ala Val Gly Gly Gln Gly Ser Glu Arg Pro  
35 40 45

Gly Asp Ala Thr Val Ile Val Thr Phe Lys Asp Gln Ser Gln Arg Ser  
50 55 60

His Phe Leu Gln Gln Val Pro Leu Pro Pro Gly Met Ser Ala His Gly  
65 70 75 80

Val Thr Met Thr Val Asp Phe  
85

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Pro Pro Val Ile Cys Leu Lys Gly Gly His Asn Gln Leu Lys Cys Leu  
1 5 10 15

Arg Tyr Arg Leu Lys Ser Lys His Ser Ser Leu Phe Asp Cys Ile Ser  
20 25 30

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Thr Thr Trp Ser Trp Val Asp Thr Thr Ser Thr Cys Arg Leu Gly Ser  
 35 40 45

Gly Arg Met Leu Ile Lys Phe Ala Asp Ser Glu Gln Arg Asp Lys Phe  
 50 55 60

Leu Ser Arg Val Pro Leu Pro Ser Thr Thr Gln Val Phe Leu Gly Asn  
 65 70 75 80

Phe Tyr Gly Leu

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Pro Val Ile Leu Val Arg Gly Gly Ala Asn Thr Leu Lys Cys Phe  
 1 5 10 15

Arg Asn Arg Ala Arg Val Arg Tyr Arg Gly Leu Phe Lys Tyr Phe Ser  
 20 25 30

Thr Thr Trp Ser Trp Val Ala Gly Asp Ser Thr Glu Arg Leu Gly Arg  
 35 40 45

Ser Arg Met Leu Ile Leu Phe Thr Ser Ala Cys Gln Arg Glu Lys Pro  
 50 55 60

Asp Glu Thr Val Lys Tyr Pro Lys Gly Val Asp Thr Ser Tyr Gly Asn  
 65 70 75 80

Leu Asp Ser Leu

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Pro	Pro	Val	Val	Cys	Val	Lys	Gly	Gly	Ala	Asn	Gln	Leu	Lys	Cys	Leu
1				5					10					15	
Arg	Tyr	Arg	Leu	Lys	Ala	Ser	Thr	Gln	Val	Asp	Phe	Asp	Ser	Ile	Ser
			20					25					30		
Thr	Thr	Trp	His	Trp	Thr	Asp	Arg	Lys	Asn	Thr	Glu	Arg	Ile	Gly	Ser
		35					40					45			
Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Asp	Glu	Ala	Gln	Arg	Glu	Lys	Phe
	50					55					60				
Leu	Glu	Arg	Val	Ala	Leu	Pro	Arg	Ser	Val	Ser	Val	Phe	Leu	Gly	Gln
65					70					75					80
Phe	Asn	Gly	Ser												

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Thr	Pro	Ile	Val	Gln	Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe
1				5					10					15	
Arg	Tyr	Arg	Leu	Asn	Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser
			20					25					30		
Ser	Thr	Trp	His	Trp	Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile
		35					40					45			
Val	Thr	Leu	Thr	Tyr	Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn
	50					55					60				



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Ser Val Lys Ile Pro Pro Thr Ile Arg His Lys Val Gly Phe Met Ser  
 65 70 75 80

Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Pro Ile Val Gln Phe Gln Gly Glu Ser Asn Cys Leu Lys Cys Phe  
 1 5 10 15

Arg Tyr Arg Leu Asn Arg Asp His Arg His Leu Phe Asp Leu Ile Ser  
 20 25 30

Ser Thr Trp His Trp Ala Ser Ser Lys Ala Pro His Lys His Ala Ile  
 35 40 45

Val Thr Val Thr Tyr Asp Ser Glu Glu Gln Arg Gln Gln Phe Leu Asp  
 50 55 60

Val Val Lys Ile Pro Pro Thr Ile Ser His Lys Leu Gly Phe Met Ser  
 65 70 75 80

Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

104

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr	Pro	Ile	Ile	His	Leu	Lys	Gly	Asp	Arg	Asn	Ser	Leu	Lys	Cys	Leu
1				5					10					15	
Arg	Tyr	Arg	Leu	Arg	Lys	His	Ser	Asp	His	Tyr	Arg	Asp	Ile	Ser	Ser
			20					25					30		
Thr	Trp	His	Trp	Thr	Gly	Ala	Gly	Asn	Glu	Lys	Thr	Gly	Ile	Leu	Thr
			35					40					45		
Val	Thr	Tyr	His	Ser	Glu	Thr	Gln	Arg	Thr	Lys	Phe	Leu	Asn	Thr	Val
			50				55				60				
Ala	Ile	Pro	Asp	Ser	Val	Gln	Ile	Leu	Val	Gly	Tyr	Asn	Thr	Met	Tyr
65					70					75				80	

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr	Pro	Ile	Val	His	Leu	Lys	Gly	Asp	Ala	Asn	Thr	Leu	Lys	Cys	Leu
1				5					10					15	
Arg	Tyr	Arg	Phe	Lys	Lys	His	Cys	Thr	Leu	Tyr	Thr	Ala	Val	Ser	Ser
			20					25					30		
Thr	Trp	His	Trp	Thr	Gly	His	Asn	Tyr	Lys	His	Lys	Ser	Ala	Ile	Val
			35				40					45			
Thr	Leu	Thr	Tyr	Asp	Ser	Glu	Trp	Gln	Arg	Asp	Gln	Phe	Leu	Ser	Gln
			50				55				60				
Val	Lys	Ile	Pro	Lys	Thr	Ile	Thr	Val	Ser	Thr	Gly	Phe	Met	Ser	Ile
65					70					75				80	

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

105

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ala	Pro	Ile	Val	His	Leu	Lys	Gly	Glu	Ser	Asn	Ser	Leu	Lys	Cys	Leu	1	5	10	15
Arg	Tyr	Arg	Leu	Lys	Pro	Tyr	Asn	Glu	Leu	Tyr	Ser	Ser	Met	Ser	Ser	20	25	30	
Thr	Trp	His	Trp	Thr	Ser	Asp	Asn	Lys	Asn	Ser	Lys	Asn	Gly	Ile	Val	35	40	45	
Thr	Val	Thr	Phe	Val	Thr	Gly	Gln	Gln	Gln	Gln	Met	Phe	Leu	Gly	Thr	50	55	60	
Val	Lys	Ile	Pro	Pro	Thr	Val	Gln	Ile	Ser	Thr	Gly	Phe	Met	Thr	Leu	65	70	75	80
Val																			

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Gly	Ile	Val	Glu	Gln	Cys	Cys	Thr	Ser	Ile	Cys	Ser	Leu	Tyr	Gln	Leu	1	5	10	15
Glu	Asn	Tyr	Cys	Asn												20			

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Ser	His	Leu	Val	Glu	Ala	Leu	Tyr
1				5					10					15	

Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Thr
			20					25					30

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gly	Ile	Val	Glu	Gln	Cys	Cys	Ala	Ser	Val	Cys	Ser	Leu	Tyr	Gln	Leu
1				5					10					15	

Glu	Asn	Tyr	Cys	Asn
				20

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Ser	His	Leu	Val	Glu	Ala	Leu	Tyr
1				5				10						15	
Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Thr		
			20				25						30		

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gln	Leu	Tyr	Ser	Ala	Leu	Ala	Asn	Lys	Cys	Cys	His	Val	Gly	Cys	Ile
1				5				10						15	
Lys	Arg	Ser	Leu	Ala	Arg	Phe	Cys								
			20												

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

108

Asp Ser Trp Met Glu Glu Val Ile Lys Ile Cys Gly Arg Glu Leu Val  
 1 5 10 15

Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Ser  
 20 25 30

Leu

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu Glu Lys Met Gly Thr Ala Lys Lys Cys Cys Ala Ile Gly Cys Ser  
 1 5 10 15

Thr Glu Asp Phe Arg Met Val Cys  
 20

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Arg Pro Asn Trp Glu Glu Arg Ser Arg Leu Cys Gly Arg Asp Leu Ile  
 1 5 10 15

Arg Ala Phe Ile Tyr Leu Cys Gly Gly Thr Arg Trp Thr Arg Leu Pro  
 20 25 30

Asn Phe Gly Asn Tyr Pro Ile Met  
35 40

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Gly Ile Val Pro Thr Leu Gln Asn Ile Val Ser Thr Val Asn Leu  
1 5 10 15

Asp Cys Lys Leu Asp Leu Lys Ala Ile Ala Leu Gln Ala Arg Asn Ala  
20 25 30

Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu  
35 40 45

Pro Lys Thr Thr Ala Leu Ile Phe Ala Ser Gly Lys Met Val Cys Thr  
50 55 60

Gly Ala Lys Ser Glu Asp Phe Ser Lys Met Ala Ala Arg Lys Tyr Ala  
65 70 75 80

Arg Ile Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Lys Asp Phe Lys  
85 90 95

Ile Gln Asn Ile Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu  
100 105 110

Glu Gly Leu Ala Tyr Ser His Ala Ala Phe Ser Ser Tyr Glu Pro Glu  
115 120 125

Leu Phe Pro Gly Leu Ile Tyr Arg Met Lys Val Pro Lys Ile Val Leu  
130 135 140

Leu Ile Phe Val Ser Gly Lys Ile Val Ile Thr Gly Ala Lys Met Arg  
145 150 155 160

Asp Glu Thr Tyr Lys Ala Phe Glu Asn Ile Tyr Pro Val Leu Ser Glu  
165 170 175

Phe Arg Lys Ile Gln Gln  
180

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asn Ser Asn Ser Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr  
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr  
20 25 30

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys  
35 40 45

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln  
50 55 60

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly  
65 70 75 80

Phe Met Ser Ile

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr  
1 5 10 15



111

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr  
                   20                  25                  30  
 Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys  
                   35                  40                  45  
 Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln  
                   50                  55                  60  
 Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly  
                   65                  70                  75                  80  
 Phe Met Ser Ile

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ser Gly Asn Thr Thr Pro Ile Ile His Leu Lys Gly Asp Arg Asn Ser  
 1                  5                  10                  15  
 Leu Lys Cys Leu Arg Tyr Arg Leu Arg Lys His Ser Asp His Tyr Arg  
                   20                  25                  30  
 Asp Ile Ser Ser Thr Trp His Trp Thr Gly Ala Gly Asn Glu Lys Thr  
                   35                  40                  45  
 Gly Ile Leu Thr Val Thr Tyr His Ser Glu Thr Gln Arg Thr Lys Phe  
                   50                  55                  60  
 Leu Asn Thr Val Ala Ile Pro Asp Ser Val Gln Ile Leu Val Gly Tyr  
                   65                  70                  75                  80  
 Met Thr Met

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid

112

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Gly Asn Thr Ala Pro Ile Val His Leu Lys Gly Glu Ser Asn Ser  
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Leu Lys Pro Tyr Lys Glu Leu Tyr Ser  
20 25 30

Ser Met Ser Ser Thr Trp His Trp Thr Ser Asp Asn Lys Asn Ser Lys  
35 40 45

Asn Gly Ile Val Thr Val Thr Phe Val Thr Glu Gln Gln Gln Gln Met  
50 55 60

Phe Leu Gly Thr Val Lys Ile Pro Pro Thr Val Gln Ile Ser Thr Gly  
65 70 75 80

Phe Met Thr Leu

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Gly Asn Thr Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln  
1 5 10 15

Val Lys Cys Tyr Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr  
20 25 30

Glu Asn Cys Thr Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu  
35 40 45

Arg Gln Gly Gln Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln  
50 55 60

Arg Gln Asp Phe Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile  
65 70 75 80

Ser Gly Phe Thr Ala Ser Leu Asp Phe  
85

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ser Asn Lys Lys Thr Thr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asn Ser Asn Thr  
1

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids

114

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Gly Asn Thr  
1

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Ser Ser Gly Ser Ser Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Cys Tyr Pro Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Glu Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
50 55 60

Thr Ala  
65

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
1 5 10 15

116

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
50 55 60

Thr Ala  
65

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
50 55 60

Thr Ala  
65

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Glu Pro Ser  
85 90 95

(i) **SEQUENCE CHARACTERISTICS:**  
 (A) **LENGTH:** 96 amino acids  
 (B) **TYPE:** amino acid  
 (D) **TOPOLOGY:** linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile  
65 70 75 80

Ala Arg Glu Ile Tyr Glu Met Cys Glu Ala Val Ser Met Glu Pro Ser  
85 90 95

(2) INFORMATION FOR SEQ ID NO:109:

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 180 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu  
1 5 10 15

Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp  
20 25 30

Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val  
35 40 45

Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe  
50 55 60

Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro  
65 70 75 80

Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala  
85 90 95

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr  
100 105 110

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr  
115 120 125

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys  
130 135 140

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln  
145 150 155 160

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly  
165 170 175

Phe Met Ser Ile  
180



## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu  
 1 5 10 15  
 Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp  
 20 25 30  
 Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val  
 35 40 45  
 Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe  
 50 55 60  
 Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro  
 65 70 75 80  
 Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala  
 85 90 95  
 Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys  
 100 105 110  
 Thr

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr  
 1 5 10 15  
 Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser  
 20 25 30  
 Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
 35 40 45  
 Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
 50 55 60  
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
 65 70 75 80  
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
 85 90 95  
 Thr Ala Ser Asn Lys Lys Thr Thr Ala Ser Ser Gly Ser Ser Gly Ser  
 100 105 110  
 Gly Ile Val Pro Gln Leu Gln Asn Ile Val Ser Thr Val Asn Leu Gly  
 115 120 125  
 Cys Lys Leu Asp Leu Lys Thr Ile Ala Leu Arg Ala Arg Asn Ala Glu  
 130 135 140  
 Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu Pro  
 145 150 155 160  
 Arg Thr Thr Ala Leu Ile Phe Ser Ser Gly Lys Met Val Cys Thr Gly  
 165 170 175  
 Ala Lys Ser Glu Glu Gln Ser Arg Leu Ala Ala Arg Lys Tyr Ala Arg  
 180 185 190  
 Val Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Leu Asp Phe Lys Ile  
 195 200 205  
 Gln Asn Met Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu Glu  
 210 215 220  
 Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu Leu  
 225 230 235 240  
 Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu Leu  
 245 250 255  
 Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg Ala  
 260 265 270  
 Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly Phe  
 275 280 285

Arg Lys Thr Thr  
290

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr  
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser  
20 25 30

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
35 40 45

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
50 55 60

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
65 70 75 80

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
85 90 95

Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys  
100 105 110

Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr  
115 120 125

Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe  
130 135 140

Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu  
145 150 155 160

Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys  
165 170 175

Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His  
180 185 190

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Ile	Lys	Thr	His	Gln	Asn	Lys	Lys	Gly	Gly	Pro	Gly	Val	Ala	Leu	Ser
		195					200					205			
Val	Gly	Thr	Leu	Pro	Leu	Asp	Ser	Gly	Ala	Gly	Ser	Glu	Gly	Ser	Gly
	210					215					220				
Thr	Ala	Thr	Pro	Ser	Ala	Leu	Ile	Thr	Thr	Asn	Met	Val	Ala	Met	Glu
	225					230				235					240
Ala	Ile	Cys	Pro	Glu	Gly	Ile	Ala	Arg	Leu	Ala	Asn	Ser	Gly	Ile	Asn
				245					250					255	
Val	Met	Gln	Val	Ala	Asp	Leu	Gln	Ser	Ile	Asn	Ile	Ser	Gly	Asn	Gly
			260					265					270		
Phe															

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln	Leu	Tyr	Ser	Ala	Leu	Ala	Asn	Lys	Cys	Cys	His	Val	Gly	Cys	Ile
1				5					10					15	
Lys	Arg	Ser	Leu	Ala	Arg	Phe	Cys	Met	Ser	Met	Arg	Gln	Arg	Ile	Thr
			20					25					30		
Leu	Lys	Asp	Tyr	Ala	Met	Arg	Phe	Gly	Gln	Thr	Lys	Thr	Ala	Lys	Asp
		35					40					45			
Leu	Gly	Val	Tyr	Gln	Ser	Ala	Ile	Asn	Lys	Ala	Ile	His	Ala	Gly	Arg
	50					55					60				
Lys	Ile	Phe	Leu	Thr	Ile	Asn	Ala	Asp	Gly	Ser	Val	Tyr	Ala	Glu	Glu
	65				70					75				80	
Val	Lys	Pro	Phe	Pro	Ser	Asn	Lys	Lys	Thr	Thr	Ala	Ser	Asn	Lys	Lys
				85					90					95	
Thr	Thr	Ala	Met	Ala	Asp	Asp	Asp	Pro	Tyr	Gly	Thr	Gly	Gln	Met	Phe
			100					105					110		

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His Leu	Asn Thr Ala Leu Thr	His Ser Ile Phe Asn Ala Glu Leu Tyr
115	120	125
Ser Pro	Glu Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu	
130	135	140
Glu Gln	Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly	
145	150	155 160
Pro Ser	His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys	
	165	170 175
Ser Tyr	Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val	
	180	185 190
Ile Val	Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His	
	195	200 205
Ser Leu	Val Gly Lys His Cys Glu Asp Gly Val Cys Thr Val Thr Ala	
210	215	220
Gly Pro	Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His	
225	230	235 240
Val Thr	Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu	
	245	250 255
Ala Cys	Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Ser Asp Leu	
	260	265 270
Ala Tyr	Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Thr Asp Arg	
	275	280 285
Glu Lys	Glu Ile Ile Arg Gln Ala Ala Val Gln Gln Thr Lys Glu Met	
290	295	300
Asp Leu	Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser	
305	310	315 320
Thr Gly	Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile	
	325	330 335
Tyr Asp	Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met	
	340	345 350
Asp Arg	Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu	
	355	360 365
Cys Asp	Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu	
370	375	380
Glu Glu	Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr	
385	390	395 400
Asp Val	His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys	
	405	410 415

Asp Val Asn Ile Thr  
420

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
50 55 60

Thr Ala Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met  
65 70 75 80

Phe His Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val  
85 90 95

Phe Gln Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln  
100 105 110

Ile Leu Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys  
115 120 125

Glu Gly Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn  
130 135 140

Lys Lys Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala  
145 150 155 160

Lys Val Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His  
165 170 175

Ala His Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val  
180 185 190

125

Thr Ala Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile  
 195 200 205  
 Leu His Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met  
 210 215 220  
 Thr Glu Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro  
 225 230 235 240  
 Asp Leu Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly  
 245 250 255  
 Asp Arg Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys  
 260 265 270  
 Glu Met Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro  
 275 280 285  
 Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp  
 290 295 300  
 Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val  
 305 310 315 320  
 Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr  
 325 330 335  
 Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr  
 340 345 350  
 Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser  
 355 360 365  
 Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys  
 370 375 380  
 Tyr Lys Asp Ile Asn Ile Thr  
 385 390

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met	Glu	Gln	Glu	Ile	Thr	Leu	Lys	Asp	Tyr	Ala	Met	Arg	Phe	Gly	Gln	1	5	10	15
Thr	Lys	Thr	Ala	Lys	Asp	Leu	Gly	Val	Tyr	Gln	Ser	Ala	Ile	Asn	Lys	20	25	30	
Ala	Ile	His	Ala	Gly	Arg	Lys	Ile	Phe	Leu	Thr	Ile	Asn	Ala	Asp	Gly	35	40	45	
Ser	Val	Tyr	Ala	Glu	Glu	Val	Lys	Pro	Phe	Pro	Ser	Asn	Lys	Lys	Thr	50	55	60	
Thr	Ala	Met	Ala	Glu	Asp	Asp	Pro	Tyr	Leu	Gly	Arg	Pro	Glu	Gln	Met	65	70	75	80
Phe	His	Leu	Asp	Pro	Ser	Leu	Thr	His	Thr	Ile	Phe	Asn	Pro	Glu	Val	85	90	95	
Phe	Gln	Pro	Gln	Met	Ala	Leu	Pro	Thr	Ala	Asp	Gly	Pro	Tyr	Leu	Gln	100	105	110	
Ile	Leu	Glu	Gln	Pro	Lys	Gln	Arg	Gly	Phe	Arg	Phe	Arg	Tyr	Val	Cys	115	120	125	
Glu	Gly	Pro	Ser	His	Gly	Gly	Leu	Pro	Gly	Ala	Ser	Ser	Glu	Lys	Asn	130	135	140	
Lys	Lys	Ser	Tyr	Pro	Gln	Val	Lys	Ile	Cys	Asn	Tyr	Val	Gly	Pro	Ala	145	150	155	160
Lys	Val	Ile	Val	Gln	Leu	Val	Thr	Asn	Gly	Lys	Asn	Ile	His	Leu	His	165	170	175	
Ala	His	Ser	Leu	Val	Gly	Lys	His	Cys	Glu	Asp	Gly	Ile	Cys	Thr	Val	180	185	190	
Thr	Ala	Gly	Pro	Glu	Asp	Cys	Val	His	Gly	Phe	Ala	Asn	Leu	Gly	Ile	195	200	205	
Leu	His	Val	Thr	Lys	Lys	Lys	Val	Phe	Glu	Thr	Leu	Glu	Ala	Arg	Met	210	215	220	
Thr	Glu	Ala	Cys	Ile	Arg	Gly	Tyr	Asn	Pro	Gly	Leu	Leu	Val	His	Pro	225	230	235	240
Asp	Leu	Ala	Tyr	Leu	Gln	Ala	Glu	Gly	Gly	Gly	Asp	Arg	Gln	Leu	Gly	245	250	255	
Asp	Arg	Glu	Lys	Glu	Leu	Ile	Arg	Gln	Ala	Ala	Leu	Gln	Gln	Thr	Lys	260	265	270	
Glu	Met	Asp	Leu	Ser	Val	Val	Arg	Leu	Met	Phe	Thr	Ala	Phe	Leu	Pro	275	280	285	



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Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp  
 290 295 300  
 Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val  
 305 310 315 320  
 Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr  
 325 330 335  
 Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr  
 340 345 350  
 Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser  
 355 360 365  
 Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys  
 370 375 380  
 Tyr Lys Asp Ile Asn Ile Thr  
 385 390

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln  
 1 5 10 15  
 Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys  
 20 25 30  
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly  
 35 40 45  
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr  
 50 55 60  
 Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys  
 65 70 75 80  
 Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr  
 85 90 95

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Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe  
 100 105 110

Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu  
 115 120 125

Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys  
 130 135 140

Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His  
 145 150 155 160

Ile Lys Thr His Gln Asn Lys Lys Gly Gly Pro Gly Val Ala Leu Ser  
 165 170 175

Val Gly Thr Leu Pro Leu Asp Ser Gly Ala Gly Ser Glu Gly Ser Gly  
 180 185 190

Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr Asn Met Val Ala Met Glu  
 195 200 205

Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu Ala Asn Ser Gly Ile Asn  
 210 215 220

Val Met Gln Val Ala Asp Leu Gln Ser Ile Asn Ile Ser Gly Asn Gly  
 225 230 235 240

Phe

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGGAMTNYCC

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## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala His Gln Asn Ser Gln Thr  
50 55 60

His Gln Ala Ser Leu Ser Lys Gln  
65 70